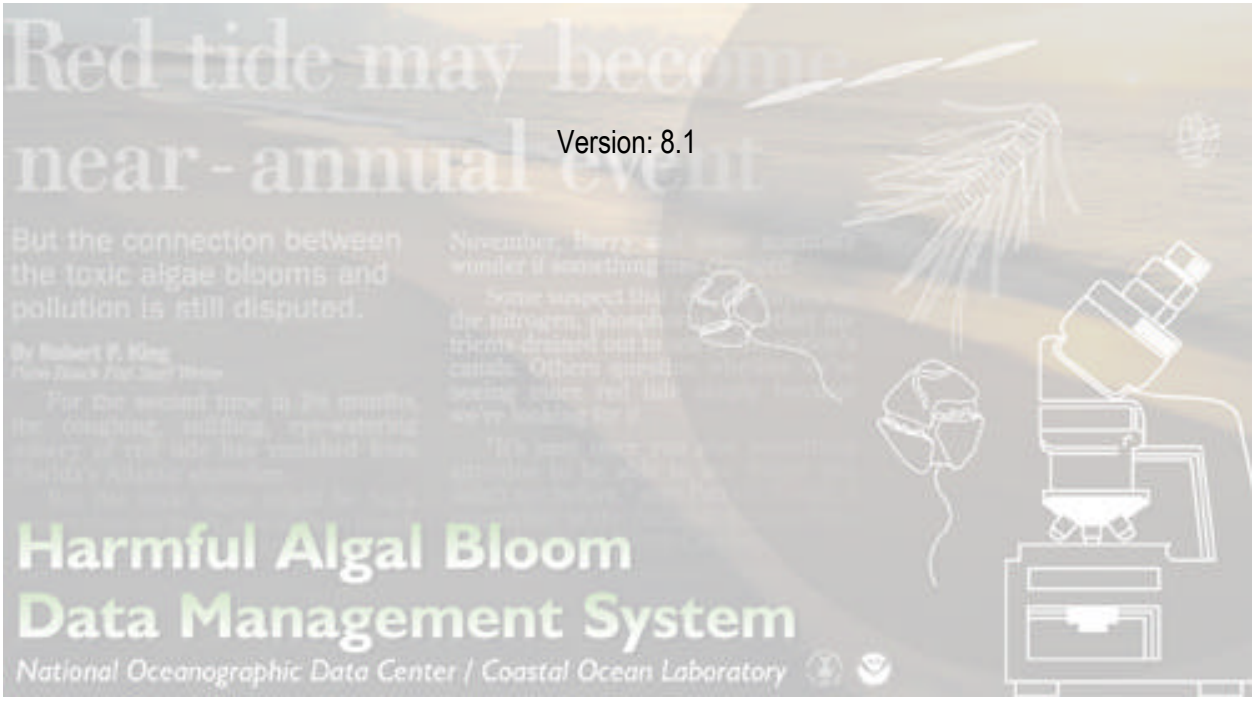
Harmful Algal Bloom Data Management System (HAB-DMS)

Exchange Format



Version: 8.1

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I. Purpose of Document

Due to the spatial extent in which harmful algal events occur, it is important to understand the ecosystem dynamics relating to these events along coasts in which multiple states border. Although many states investigate harmful algal events, there is generally little collaboration towards the integration of these disparate data sources. Therefore, a data format has been developed at the NODC to facilitate the exchange and integration of data between multiple state and academic programs. In addition, software will be developed from this format for loading data into the Harmful Algal Bloom Data Management System (HAB-DMS). To provide timely access to data from the HAB-DMS, this exchange format should be used for data submission to the NODC. In addition, an FGDC compliant metadata file should accompany any data submissions to NODC. For guidelines in preparing FGDC compliant metadata, visit FGDC's website at: http://www.fgdc.gov/metadata/metadata.html . The purpose of this document is to provide background information regarding the structure of the database tables and to discuss the exchange format in which data should be submitted to the NODC. In addition, data retrieved from the HAB database will be provided in this format.

II. Database Description

A detailed description of the structure of the HAB database, with information regarding each table, can be found on our website at: http://www.nodc.noaa.gov/col/projects/habs/docs.html . A brief description has been included within this document in order to demonstrate the structure and fields by which the data are stored. A "record" in the exchange format is used to load each table, which represents a particular stage in the process of collecting and analyzing HAB measurements (Table 1). Since each data set is unique in the types of metadata which are associated with a measurement we have structured the database so that it is flexible in the amount of information that will be stored per data entry. We encourage data providers to submit as much information as possible, in the exchange format, so that the data are useful to other users. Most of the tables contain a remark field in which additional information about the dataset can be stored.

Table 1. A summary of each table in the HAB database and the types of data they contain.

Table	Data Types
EVENT	General information regarding a data submission (NODC accession)
COLLECTION	The where, when and how a sample was collected from the water column
ANALYSIS	Further describes methods used in the chemical analysis of a sample.

RESULT	Contains further descriptive and taxonomic information regarding a biological measurement, as well as all parameters

The following discussion describes the structure of the individual database tables.

EVENT Table

Data submitted to the NODC may be representative of various time and spatial scales. One submission is considered an accession and gets a unique number for archival purposes. The EVENT table summarizes some general information regarding the entire data set (the who, where and when for the entire accession).

Name	Format	Description
event_no	number	random number created by the database when data is loaded *(leave blank in format)*
project_no	number	project code: see project code table
cruise_no	number	cruise code: see cruise code table
investigator_no	number	investigator code (the person who submitted data): see investigator code table
source	char	institute code: see institute code table
region	char	custom-defined geographical region code: see region code table
site_type	char	fixed, or random site: see site_type code table
start_date	date/time	event start date (YYYYMMDD)
end_date	date/time	event end date (YYYYMMDD)
accession_no	char	accession number assigned by NODC (7 digits)
remark	memo	remark, other miscellaneous information entered during ingest (unlimited length text field)

COLLECTION Table

Each row of the COLLECTION table contains information pertaining to where, when, and how a

sample was collected, at the station level.

Name	Format	Description
event_no	number	random number created by the database when data is loaded *(leave blank in format)*
collection_no	number	random number created by the database when data is loaded *(leave blank in format)*
station_no	number	station code: see station code table
latitude	char	latitude of collection location +/-DD.DDDDD (- is south)
longitude	char	longitude of collection location +/-DDD.DDDDD (- is west)
ll_datum	char	ll_datum code: see ll_datum table
start_date	date/time	start date of collection
start_time	char	start time of collection
end_date	date/time	end date of collection
end_time	char	end time of collection
tow_distance	number	distance of tow/haul in meters
upper_depth	number	upper depth of sample collection
lower_depth	number	lower depth sample collection
z_unit	number	unit code: see unit code table
total_depth	number	total station depth
sample_depth	number	depth of sample collection
sample_code	char	originator's sample code/number
remark	memo	remark, other miscellaneous information entered during ingest (unlimited length text field)

ANALYSIS Table

This table contains information regarding samples that are further analyzed within a laboratory. It describes how the sample was analyzed, who analyzed it, etc.

Name	Format	Description
event_no	number	random number created by the database when data is loaded *(leave blank in format)*
analysis_no	number	random number created by the database when data is loaded *(leave blank in format)*
data_type	char	bio, che, env to represent biological, chemical or environmental data type
parameter_no	number	parameter code: see parameter code table
layer	char	layer code: see layer code table
unit_no	number	unit code: see unit code
lab	number	institute code: see institute code table
investigator_no	number	investigator code: see investigator code table
gear_no	number	gear code: see gear code table
method_no	number	method code: see method code table
qualifier	char	parameter detection limit qualifier code: see detection limit qualifier code table
remark	memo	remark, other miscellaneous information entered during ingest (unlimited length text field)

RESULT Table

The RESULT table further breaks the biological parameters down by sex, life_stage, etc. Chemical and biological parameter values, such as biomass, counts etc. are stored within this table, along with the units that are associated with that measurement. A remark field is also available if further description is needed.

Name	Format	Description
event_no	number	random number created by the database when data is loaded *(leave blank in format)*
collection_no	number	random number created by the database when data is loaded *(leave blank in format)*

analysis_no	number	random number created by the database when data is loaded *(leave blank in format)*
tsn	number	taxonomy code: see taxonomy code table
value	number	parameter value
bio_group_no	number	biological group code: see Bio_group code table
life_stage_no	number	life_stage code: see life stage code table
sex_no	number	sex code: see sex code table
modifier	char	taxonomic modifier (e.g., sp, spp) text (up to 3 characters)
remark	memo	remark, other miscellaneous information entered during ingest (unlimited length text field)

III. HAB-DMS Exchange Format

The format that has been developed by the NODC for data entry into the HAB database has been designed to provide information regarding the collection and laboratory phases of data acquisition, associated with each chemical and biological parameter. This format was developed by the NODC to provide enough flexibility for data providers, while still maintaining some consistency in formatting. The HAB-DMS exchange format was designed to work well with spreadsheet or columnar data. Codes for data elements should be consistent with the NODC HAB-DMS codes, which were designed to match CIMS 2000 (see http://www.chesapeakebay.net/data/index.htm) codes wherever possible. If a desired entry is not found in a HAB-DMS code table, place the full text within the format and one will be assigned by the NODC. Although submission of data with the appropriate NODC HAB-DMS codes is desired and will facilitate entry into the HAB database, data will be accepted with text descriptions of these coded values. Additional information can be added to the parameter records, as they pertain to the table structure (e.g., if additional information is available regarding the lifestage, sex, tow_distance, etc of a biological measurement, this information should be stored at the data level, with the appropriate header to describe the field). We have used a colon to separate field names with the data, to avoid any confusion regarding the beginning of a record. Each new record should be entered on a new line, where multiple entries of the same record type may follow on consecutive lines (e.g., if more than one Principal Investigator was responsible for the project, multiple entries (rows) should be entered to completely describe the data set). Field names should be spelled out (no=number, #=number) to avoid any discrepancies prior to loading. We prefer that data submitted to NODC is pipe or comma delimited, however, any delimiter can be used as long as it is described within the *file info* record.

Due to the difficulty in handling biological data types, we have created two variations of this format for data that contains single species (or taxon group) data, and those that contain estimates of multiple species. When dealing with biological data which contains a single species, the data should be treated similar to the chemical data, and use the same format (wherein the biological parameter info record contains all of the information pertaining to the column of biological data). However, in cases where the taxonomic information varies within the data itself, the taxonomic serial number (or scientific name) and biological grouping codes should be provided within the data, with an appropriate header.

I. File Information Block

A. Format

<file info>
original file: *name of the original file*
current file: *name of the file actually converted after titles, etc. are cut out*
converter: *program used to convert into this format*

delimiter: *the character used to separate columns of data*

B. Description

The delimiter character must be used to delimit items in <environment info>, <station info>, <chemical parameter info>, <biological parameter info>, <header info>, and <data> blocks. A character that is not found in any remark columns must be used.

II. Event Information Block

A. Format

<event info>
project: *project code: see project code table*
cruise: *cruise code: see cruise code table*
investigator: *investigator code (the person who submitted data): see investigator code table*
source: *institute code: see institute code table*
region: *custom-defined geographical region code: see region code table*
site type: *fixed, or random site: see site_type code table*
accession number: *accession number assigned by NODC (7 digits)-Leave blank*
start date: *event start date (YYYYMMDD)*
end date: *event end date (YYYYMMDD)*
remark: *remark, other miscellaneous information entered during ingest: text field*

III. Environment Information Block

A. Format

<**environment info**>
column number(start with 0)|parameter code|units|remarks

B. Description

1. **<environment info>** - indicates the beginning of the <environment info> block and followed by environment information row(s)
2. **column number** - column position in <data> block, beginning with 0.
3. **parameter code** - parameter code present in Parameter table.
4. **unit** - unit code present in Unit table, unit used for parameter measurement.
5. **remark** - remark less than 256 characters.

The environment information block is used to store information regarding station level parameters pertaining to weather and/or surface conditions. If a column doesn't exist in both <header> and <data> block, the program will generate an error message and stop. If both parameter code and unit code were not found in the corresponding table, the corresponding row will not be loaded into database.

IV. Station Information Block

A. Format

<station info> *This information should be provided one time, and when station locations change for a program.
station id|*latitude*|*longitude*|*ll_datum*|*program*|*remark*

B. Description

1. **<station info>** - indicates the beginning of the <station info> block and followed by station information row(s)
2. **station id** - An existing station id in Station table. If not found, the program will generate an error message and stop.
3. **latitude** - value of latitude column in Station table
4. **longitude** - value of longitude column in Station table
5. **ll_datum** - value of ll_datum column in Station table
6. **program** - value of program column in Station table
7. **remark** - value of remark column in Station table

The values of 'latitude', 'longitude', 'll_datum', 'program', and 'remark' columns correspond to those of the corresponding columns in the Station table.

V. Chemical Parameter Information Block

A. Format

<chemical parameter info>
column number(start with 0)|*parameter*
code|*layer*|*units*|*qualifier*|*lab*|*investigator*|*gear*|*method*|*remark*

B. Description

1. **<chemical parameter info>** - indicates the beginning of the <chemical parameter info> block and followed by chemical parameter information row(s)
2. **column number** - column position in <data> block, beginning with 0. The program

will generates an error message and stop for any duplicate column number or non-existing column.

3. **parameter code** - parameter code present in Parameter table.
4. **layer** - "S" for surface, "B" for bottom, "AP" for above pycnocline, "BP" for below pycnocline, or "M" for mid-depth. "UNKNOWN" will be stored, if not provided.
5. **unit** - unit code present in Unit table, unit used for parameter measurement.
6. **qualifier** - qualifier
7. **lab** - name of the institute present in Institute table, the lab that performed analysis on the parameter
8. **investigator** - name of the investigator present in Investigator table (Format: Last, First Middle), lab analyst/technician
9. **gear** - gear model present in Gear table, gear used to measure the parameter
10. **method** - method code present in Method table, method used to measure the parameter
11. **remark** - remark less than 256 characters.

Identical parameter codes are allowed as long as parameter factors combined (layer, unit, lab, investigator, gear, and method) are unique.

VI. Biological Parameter Information Block for Single or no Taxon

A. Format

<biological parameter info> ** For data which contains measurements for a single taxon
column number(start with 0)|parameter code|tsn|bio_group|life_stage|sex|modifier|layer|units|qualifier|lab|investigator|gear|method|remark

B. Description

1. **<biological parameter info>** - beginning of the <biological parameter info> block and followed by biological parameter information row(s)
2. **column number** - column position in <data> block, beginning with 0. The program will generate an error message and stop for any duplicate column number or non-existing column.
3. **parameter code** - parameter code present in Parameter table.
4. **tsn** - Either the seven digit taxonomy code present in the taxonomy table or the scientific name may be used in this field. It must contain the tsn code for the corresponding tsn description in the corresponding <header> block column.
5. **bio group** - biological group present in Bio_Group table. It is optional, but '0' (unknown) will be loaded if its value was not found in the table.

6. **life stage** - If applicable, enter the life stage of the organism present in the Life_stage table.
7. **sex** - If applicable, enter the sex of the organism present in the Sex table.
8. **modifier** - If applicable, enter any modifiers to the scientific name of the organism (e.g., spp., sp., etc).
7. **layer** - "S" for surface, "B" for bottom, "AP" for above pycnocline, "BP" for below pycnocline, or "M" for mid-depth. "UNKNOWN" will be loaded, if not provided.
8. **unit** - unit code present in Unit table, unit used for parameter measurement
9. **qualifier** - qualifier
10. **lab** - name of the institute present in Institute table the lab that performed analysis on the parameter
11. **investigator** - investigator name present in Investigator table (Format: Last, First Middle), lab analyst/technician
12. **gear** - gear model present in Gear table, gear used to measure the parameter
13. **method** - method code present in Method table, method used to measure the parameter
14. **remark** - remark less than 255 characters.

Identical parameter codes are allowed as long as parameter factors combined (layer, unit, lab, investigator, gear, and method) are unique.

VII. Biological Parameter Information Block for Multiple Taxa

A. Format**:** This format should be used for data which contains measurements for multiple taxa (where *tsn* and *bio_group* will be provided within the data with the appropriate column labeled in the header)

<biological parameter info>
column number(start with 0)|parameter
code|layer|units|qualifier|lab|investigator|gear|method|remark

B. Description

1. **<biological parameter info>** - indicates the beginning of the <biological parameter info> block and followed by biological parameter information row(s)
2. **column number** - column position in <data> block, beginning with 0. The program will generate an error message and stop for any duplicate column number or non-existing column.
3. **parameter code** - parameter code present in Parameter table. If not found, the program will generate an error message and stop.
4. **layer** - "S" for surface, "B" for bottom, "AP" for above pycnocline, "BP" for below pycnocline, or "M" for mid-depth. "UNKNOWN" will be loaded, if not provided.

5. **unit** - unit code present in Unit table, unit used for parameter measurement
6. **qualifier** - qualifier
7. **lab** - name of the institute present in Institute table, the lab that performed analysis on the parameter
8. **investigator** - investigator name present in Investigator table, (Format: Last, First Middle) lab analyst/technician
9. **gear** - gear model present in Gear table, gear used to measure the parameter
10. **method** - method code present in Method table, method used to measure this parameter
11. **remark** - remark less than 255 characters

Both "tsn" and "bio group" columns must be present in <header info> block and their corresponding values must be present in <data> block. Otherwise, the program will generate an error message and stop. It is possible to have identical parameter codes as long as parameter factors combined (layer, unit, lab, investigator, gear, and method) are unique. Any unprovided parameter will be stored as "UNKNOWN" in database.

VIII. Header Information Block

A. Format

<header info>

parameter 1|*parameter 2*| ... |*parameter n*

B. Description

<header info> - indicates the beginning of the <header info> block.

General parameters, specific biological parameters and the parameters described in <environment info>, <chemical parameter info>, and <biological parameter info> block(s) must be present in the <header info> block. In the current version of the database, general parameters include: station code, latitude/longitude, ll datum, collection start date, collection end date, collection start time, collection end time, tow distance, upper depth, lower depth, total depth, sample depth, sample code, z unit and remark. Specific biological parameters, which can be used to describe data with multiple taxa, may include: tsn, biological group, life stage, sex and modifier. Minimal collection location information must exist, or the program will generate an error message and stop. There must exist either a station id column or latitude and longitude columns. Minimal collection date information must exist, or the program will generate an error message and stop. Start date is required, but end date, start time, and end time are optional. The date values in the

<data> block must be in “MM/DD/YY”, “MM/DD/YYYY”, “YYYY/MM/DD”, or “YYYYMMDD” format. If the end date is not present, the program will assign the value of start date to it. The time values in the <data> block must in either “MM:SS” or “MMSS”, where MM is a valid minute value and SS is a valid second value. If the start time is present and the end time is not, the program will assign the value of the start to it. If any environmental, chemical, or biological parameter which is not described in the corresponding block is present, the program will simply ignore it. If a parameter which is described in the corresponding block is not present, the program will generate an error message and stop. Even though not required, it is strongly recommended for quality control purposes that the parameter codes used in the parameter information blocks be used in the <header info> block.

IX. Data Block

A. Format

<data>
delimited version of the spreadsheet contents

B. Description

<data> - indicates the beginning of the <data> block.

If the number of columns in this block doesn’t match that in the <header info> block, the program will generate an error message and stop. If an invalid bio group exists, the program will generate an error message and stop. If an invalid date, station id, or latitude/longitude exists, the program will generate an error message and stop. But, any other invalid parameter value will be ignored and won’t be loaded.

IV. Sample Chemical Data Set

A sample of DE-DNREC Pfiesteria monitoring data in MS Excel format was used to demonstrate the use of the HAB-DMS exchange format. The original has more parameters extending to the right, and more stations below. The following data set is a subset which represents chemical data from the DE-DNREC Pfiesteria monitoring program.

Station	ESS Sample Number	Date Sampled	Time Sampled	Total Depth	TSS	Chl-a	TP
I-1	98013400	5/5/98	10:27		47.0	5.0	0.084
I-1		5/19/98	9:25	10.0	39.0	8.0	0.14
I-1	98018300	6/9/98	11:00	4.5	33.0	3.0	0.152
I-1	98021660	6/22/98	12:00	3.5	43.0	3.0	0.114

I-1	98025130	7/6/98	9:53	5.5	74.0	3.0	0.204
I-1	98029630	7/22/98	11:00	5.5	40.0	8.0	0.446
I-1	98033300	8/5/98	15:50	3.5	33.0	5.0	0.076
I-1	98036070	8/18/98	10:58	6.0	135.0	11.0	0.098
I-1	98038570	8/31/98	11:15	5.5	147.0	16.0	0.456
I-1	98041640	9/14/98	12:35	5.0	114.0	8.0	0.078
I-1	98044690	9/30/98	10:40	5.0	120.0	5.0	
I-1	98049300	10/21/98	11:00	5.8	31.0	8.0	
IP-1	98013490	5/5/98	13:06	6.0	38.0	24.0	0.121

Sample of Format: Using the same spreadsheet data above.

*** Note that the following format assumes that the latitude/longitude coordinates for each station has been provided to NODC in a previous data submission.**

<file info>
original file: rt990212.xls
current file: /disk4/hab/data/testdata.csv
converter: de_p1.pro
delimiter: pipe
<event info>
project: DE-DNREC Pfiesteria Monitoring
cruise:
investigator: Edythe Humphries
source: DE-DNREC
region: Chesapeake
site type: fixed
accession number: 0000001
start date:19980505
end date: 19981021
remark: sample dataset - testing only
<chemical parameter info>
4|TSS|S|mg/l||DNREC-ELS-ASB|Kathy Knowles||TSS|
5|CHLA|S|ug/l||DNREC-ELS-ASB|Dave Saveikis||PHEO1|
6|TP|B|mg/l||DNREC-ELS-ASB|Kathy Knowles||PHOS1|
<header info>
station id|sample no|date|time|total depth|TSS|CHLA|TP
<data>
I-1|98013400|5/5/98|10:27||47.0|5.0|0.084
I-1||5/19/98|9:25|10.0|39.0|8.0|0.14
I-1|98018300|6/9/98|11:00|4.5|33.0|3.0|0.152
I-1|98021660|6/22/98|12:00|3.5|43.0|3.0|0.114
I-1|98025130|7/6/98|9:53|5.5|74.0|3.0|0.204
I-1|98029630|7/22/98|11:00|5.5|40.0|8.0|0.446

I-1|98033300|8/5/98|15:50|3.5|33.0|5.0|0.076
I-1|98036070|8/18/98|10:58|6.0|135.0|11.0|0.098
I-1|98038570|8/31/98|11:15|5.5|147.0|16.0|0.456
I-1|98041640|9/14/98|12:35|5.0|114.0|8.0|0.078
I-1|98044690|9/30/98|10:40|5.0|120.0|5.0|
I-1|98049300|10/21/98|11:00|5.8|31.0|8.0|
IP-1 |98013490|5/5/98|13:06|6.0|38.0|24.0|0.121

V. Sample Biological Data Set (without taxonomic information)

The following data set represents a subset of data from DE-DNREC's Pfiesteria monitoring program. It represents data which contains biological information, however, the biological data is not analyzed to the taxonomic level (does not contain a tsn). Therefore, PLO is identified as a bio_group in this format.

Station	ESS Sample Number	Date Sampled	Time Sampled	Total Depth	PLO (#/ml)	Code	Analyst
I-1	98013400	5/5/98	10:27			None	EH
I-1		5/19/98	9:25	10.0		None	EH
I-1	98018300	6/9/98	11:00	4.5	10		GMM
I-1	98021660	6/22/98	12:00	3.5		None	GMM
I-1	98025130	7/6/98	9:53	5.5	10		GMM
I-1	98029630	7/22/98	11:00	5.5		None	GMM
I-1	98033300	8/5/98	15:50	3.5		None	GMM
I-1	98036070	8/18/98	10:58	6.0		None	GMM
I-1	98038570	8/31/98	11:15	5.5		None	GMM
I-1	98041640	9/14/98	12:35	5.0		None	GMM
I-1	98044690	9/30/98	10:40	5.0		None	GMM

<file info>
original file: rt990212.xls
current file: /disk4/hab/data/testdata.csv
converter: de_p2.pro
delimiter: pipe
<event info>
project: DE-DNREC Pfiesteria Monitoring
cruise:
investigator: Edythe Humphries
source: DE-DNREC
region: Chesapeake
site type: fixed
accession number: 0000002
start date:19980505
end date: 19981021

remark: sample dataset - testing only
<biological parameter info>
5|COUNT||PLO||||S|number/ml||DNREC-ELS-ASB|Edythe Humphries|Whole Water Column Sampler|PLO1|a value of 0 indicates that no Pfiesteria like organisms were observed in 0.1 ml subsample of Lugol's preserved 125 ml sample
<header info>
station id|sample number|date|time|total depth|PLO
<data>
I-1|98013400|5/5/98|10:27|10|0
I-1||5/19/98|9:25|4.5|0
I-1|98018300|6/9/98|11:00|3.5|10
I-1|98021660|6/22/98|12:00|5.5|0
I-1|98025130|7/6/98|9:53|5.5|10
I-1|98029630|7/22/98|11:00|3.5|0
I-1|98033300|8/5/98|15:50|6.0|0
I-1|98036070|8/18/98|10:58|5.5|0
I-1|98038570|8/31/98|11:15|5.0|0
I-1|98041640|9/14/98|12:35|5.0|0
I-1|98044690|9/30/98|10:40|0

VI. Sample Biological Data Set (with taxonomic information for a single taxon)

The following example represents sample data collected during the January 1999 ECOHAB-Florida cruise and was provided by Dr. Gabe Vargo for use in the development of the HAB database at NODC. It represents a biological data set which also contains taxonomic information, for a single species.

DATE	TIME	LAT	LONG	Station	Depth (m)	G. breve (cells/l)	
1/13/1999		4:17	27.465	-82.966	3	0	0
1/13/1999		4:17	27.465	-82.966	3	13	0
1/13/1999		2:54	27.389	-83.134	5	0	0
1/13/1999		2:54	27.389	-83.134	5	25	0
1/13/1999		1:26	27.314	-83.301	7	0	0
1/13/1999		1:26	27.314	-83.301	7	30	0
1/13/1999		23:59	27.238	-83.468	9	0	0
1/13/1999		23:10	27.2	-83.552	10	0	0
1/13/1999		23:10	27.2	-83.552	10	40	0
1/13/1999		15:57	26.472	-84.392	11	0	0

<file info>

original file: eh0199gbreveconcentration.txt
current file: /disk4/hab/data/tabgbreve.txt
converter: gbreve_sample.pro
delimiter: comma
<event info>
project:ECOHAB-Florida
cruise: EH0199
investigator: Dr. Gabriel Vargo
source: Department of Marine Science, University of South Florida
region: Gulf of Mexico
site type: random
accession number: 0000003
start date:19990113
end date: 19990113
remark: sample dataset - testing only
<biological parameter info>
6,COUNT,0010157,Dinoflagellate,,,,,number/liter,,USF,Dr. Gabriel Vargo,rosette sampler,Preserved in Lugols solution. Cell abundance was determined by microscopic counts,
<header info>
date,time,latitude,longitude,station,depth,G. breve
<data>
1/13/1999,4:17,27.465,-82.966,3,0,0
1/13/1999,4:17,27.465,-82.966,3,13,0
1/13/1999,2:54,27.389,-83.134,5,0,0
1/13/1999,2:54,27.389,-83.134,5,25,0
1/13/1999,1:26,27.314,-83.301,7,0,0
1/13/1999,1:26,27.314,-83.301,7,30,0
1/13/1999,23:59,27.238,-83.468,9,0,0
1/13/1999,23:10,27.2,-83.55210,0,0
1/13/1999,23:10,27.2,-83.55210,40,0
1/13/1999,15:57,26.472,-84.392,11,0,0

VII. Sample Biological Data Set (with taxonomic information for multiple taxa)

The following data set represents data provided through the NECOP program in 1990, which were collected by Dr. Nancy Rabalais. It represents estimates of biological diversity and abundance of benthic organisms at several stations off the Louisiana coast.

MONTH,YEAR,SITE,STATION,DEPTH_CORE,REPL,GENUS,SPECIES,NUMBER,TAXA
09,90,SH,1000,0,A,Magelona,sp. H,1,Polychaeta
09,90,SH,1000,0,A,Malacoceros,vanderhorsti,1,Polychaeta

09,90,SH,1000,0,A,Nemertea,sp. A,2,Nemertea
09,90,SH,1000,0,A,Nuculana,concentrica,3,Bivalvia
09,90,SH,1000,0,A,Paramphinome,sp. B,1,Polychaeta
09,90,SH,1000,0,A,Paraprionospio,pinnata,12,Polychaeta
09,90,SH,1000,0,A,Prionospio,delta,2,Polychaeta
09,90,SH,1000,0,A,Sigambra,tentaculata,3,Polychaeta

<file info>
original file: ben90a.csv
current file: ben90a.csv.out
converter: exchange.pro
delimiter: comma
<event info>
project: NECOP
cruise:
investigator: Jim Hendee
source: AOML
region: Gulf of Mexico
site type: F
accession number: 9800129
start date: 19900901
end date: 19901001
remark:
<biological parameter info>
5,COUNT,SE,number/sample,,LUMCON,Nancy Rabalais,EKMAN,COUNT,samples were taken with a 0.023 m^2 Ekman grab. The animals obtained were those retained on a 0.5 mm sieve. Standard techniques include shipboard preservation in 10% buffered formalin stained with rose bengal. Identification and enumeration to lowest possible taxon.
<header info>
DATE,STATION ID,TOTAL DEPTH,SAMPLE NUMBER,TSN,NUMBER,BIO GROUP,REMARK
<data>
09/19/90,SH-1000,0.1,A,Magelona,1,Polychaeta,sp. H
09/19/90,SH-1000,0,A,Malacoceros vanderhorsti,1,Polychaeta,
09/19/90,SH-1000,0,A,Nemertea,2,Nemertea,sp. A
09/19/90,SH-1000,0,A,Nuculana concentrica,3,Bivalvia,
09/19/90,SH-1000,0,A,Paramphinome,1,Polychaeta,sp. B
09/19/90,SH-1000,99.02,A,Paraprionospio pinnata,12,Polychaeta,
09/19/90,SH-1000,0,A,Prionospio delta,2,Polychaeta,
09/19/90,SH-1000,0,A,Sigambra tentaculata,3,Polychaeta,